```
FILE 'REGISTRY' ENTERED AT 09:24:35 ON 17 DEC 2001

=> S 2.7.8.17

L1             1 2.7.8.17

=> D


L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2001 ACS
RN   84012-69-1  REGISTRY
CN   Acetylglucosamine-1-phosphotransferase, uridine diphosphoacetylglucosamine-
     lysosomal enzyme precursor (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Acetylglucosamine-1-phosphotransferase, uridine diphosphoacetylglucosamine-
     glycoprotein
CN     ***E.C. 2.7.8.17***
CN   Lysosomal enzyme acetylglucosamine-1-phosphotransferase
CN   Lysosomal enzyme N-acetylglucosamine-1-phosphotransferase
CN   Lysosomal enzyme precursor acetylglucosamine-1-phosphotransferase
CN   N-Acetylglucosaminyl phosphotransferase
CN   UDP-acetylglucosamine:lysosomal enzyme precursor acetylglucosamine-1-
     phosphotransferase
CN   UDP-GlcNAc:lysosomal enzyme N-acetylglucosamine-1-phosphotransferase
CN   UDP-N-acetylglucosamine:glycoprotein N-acetylglucosamine-1-
     phosphotransferase
CN   UDP-N-acetylglucosamine:glycoprotein N-acetylglucosaminyl-1-
     phosphotransferase
DR   78169-43-4
MF   Unspecified
CI   MAN
LC   STN Files:   BIOSIS, CA, CAPLUS, TOXCENTER, TOXLIT

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
               54 REFERENCES IN FILE CA (1967 TO DATE)
               54 REFERENCES IN FILE CAPLUS (1967 TO DATE)


=> S 3.1.4.45

L2             1 3.1.4.45

=> D


L2   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2001 ACS
RN   75788-84-0  REGISTRY
CN   Phosphodiesterase, .alpha.-acetylglucosaminyloligosaccharide (9CI)  (CA
     INDEX NAME)
OTHER NAMES:
CN   .alpha.-N-Acetyl-D-glucosamine-1-phosphodiester N-acetylglucosaminidase
CN   .alpha.-N-Acetylglucosaminyl phosphodiesterase
CN     ***E.C. 3.1.4.45***
CN   Lysosomal .alpha.-N-acetylglucosaminidase
CN   N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase
CN   N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase
MF   Unspecified
CI   MAN
LC   STN Files:   BIOSIS, CA, CAPLUS, TOXCENTER

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
               33 REFERENCES IN FILE CA (1967 TO DATE)
               33 REFERENCES IN FILE CAPLUS (1967 TO DATE)

FILE 'CAPLUS' ENTERED AT 09:26:02 ON 17 DEC 2001

=> S ACETYLGLUCOSAMINE(4W)PHOSPHOTRANSFERASE

          10038 ACETYLGLUCOSAMINE
           6792 PHOSPHOTRANSFERASE
L3          118 ACETYLGLUCOSAMINE(4W)PHOSPHOTRANSFERASE

=> S PHOSPHODIESTERASE(3W)ACETYLGLUCOSAMIDASE

          20579 PHOSPHODIESTERASE
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          53 ACETYLGLUCOSAMIDASE
L4         0 PHOSPHODIESTERASE(3W)ACETYLGLUCOSAMIDASE

=> S PHOSPHODIESTERASE(3A)ACETYLGLUCOSAMINE

       20579 PHOSPHODIESTERASE
       10038 ACETYLGLUCOSAMINE
L5         4 PHOSPHODIESTERASE(3A)ACETYLGLUCOSAMINE

=> S L3 OR L1

          79 L1
L6       148 L3 OR L1

=> S L2 OR L5

          33 L2
L7        34 L2 OR L5

=> S LYSOM?

L8       199 LYSOM?

=> S LYSOSOM?

L9     30729 LYSOSOM?

=> S L9 AND (L6,L7)

L10       96 L9 AND ((L6 OR L7))

=> S HYDROLASE

L11    15397 HYDROLASE

=> S L10 AND L11

L12       11 L10 AND L11

=> S L6 AND L7

L13       19 L6 AND L7

=> S L12,L13

L14       26 (L12 OR L13)

=> D 1-26 CBIB ABS


L14  ANSWER 1 OF 26  CAPLUS  COPYRIGHT 2001 ACS
2001:300891  Document No. 134:322353  Post-translational modification of
     recombinant proteins in plants by altering its natural modification
     abilities.  Russell, Douglas; Manjunath, Siva; Bassuner, Ronald (Monsanto
     Company, USA).  PCT Int. Appl. WO 2001029242 A2 20010426, 132 pp.
     DESIGNATED STATES: W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ,
     CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,
     HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
     LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG,
     SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY,
     KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE,
     DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN,
     TD, TG.  (English).  CODEN: PIXXD2.  APPLICATION: WO 2000-US29027
     20001020.  PRIORITY: US 1999-PV160758 19991021; US 2000-PV195282 20000407.
AB   The present invention is directed to methods for producing a
     post-translationally modified heterologous polypeptide in a plant host
     system by altering the natural post-translational abilities of that plant
     host system.  The post-translational modification may be proteolytic
     cleavage, glycosylation, phosphorylation,methylation, sulfation,
     prenylation, acetylation, N-amidation, oxidn., hydroxylation, or
     myristylation.  In a preferred embodiment, this method includes
     transforming a plant host system with a nucleic acid that encodes a
     heterologous polypeptide, and isolating that polypeptide from the plant
     host system.  The heterologous proteins may include antibodies and
     antibody fragments, collagen types I-XX, human protein C, and cytokines.
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In another aspect of this method, altering the natural post-translational modifications is done by transforming the plant host system with one or more nucleic acid sequences encoding a post-translational modification enzyme. Such plant specific post-translational modifying enzymes include Galactosyl transferase, xylosyl transferase, and fucosyl transferase. In an alternative aspect, the altering is done by mutagenesis of plant host system. In another embodiment, the altering is done by transforming said plant host system with an expression vector comprising a nucleic acid sequence that encodes an antisense nucleic acid. The invention further provides a method for producing a post-translationally modified heterologous polypeptide in a plant host system, by cross-pollinating a first plant, wherein the plant has been transformed with a first expression vector comprising a nucleic acid sequence encoding a heterologous polypeptide, and a second plant wherein the second plant has been transformed with a second expression vector comprising a nucleic acid sequence encoding a post-translational modifying enzyme.

L14 ANSWER 2 OF 26 CAPLUS COPYRIGHT 2001 ACS
2001:208390 Document No. 134:248843 Use of GlcNAc-phosphotransferase and phosphodiester .alpha.-GlcNAcase in production of highly phosphorylated ***lysosomal*** hydrolases useful in treatment of ***lysosomal*** storage diseases. Canfield, William M. (USA). PCT Int. Appl. WO 2001019955 A2 20010322, 91 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 2000-US21970 20000914. PRIORITY: US 1999-PV153831 19990914.

AB The ***lysosomal*** targeting pathway enzymes GlcNAc-phosphotransferase and phosphodiester .alpha.-GlcNAcase and uses in prodn. of highly phosphorylated ***lysosomal*** hydrolases that can be used to treat ***lysosomal*** storage diseases, are disclosed. Generally, the nucleic acid mols. coding for the enzymes are incorporated into expression vectors that are used to transfect host cells that express the enzymes. The expressed enzymes are recovered using monoclonal antibodies capable of selectively binding to bovine GlcNAc-phosphotransferase and to bovine phosphodiester .alpha.-GlcNAcase. ***Lysosomal*** hydrolases having high mannose structures are treated with GlcNAc-phosphotransferase and phosphodiester .alpha.-GlcNAcase resulting in the prodn. of asparagine-linked oligosaccharides that are highly modified with mannose 6-phosphate ("M6P"). The treated ***hydrolase*** binds to M6P receptors on the cell membrane and is transported into the cell and delivered to the ***lysosome*** where it can perform its normal or a desired function. The highly phosphorylated ***lysosomal*** hydrolases are readily taken into the cell and into the ***lysosome*** during enzyme replacement therapy procedures.

L14 ANSWER 3 OF 26 CAPLUS COPYRIGHT 2001 ACS
2000:384553 Document No. 133:28245 Diagnosis of human glycosylation disorders. Marth, Jamey D.; Freeze, Hudson H. (The Regents of the University of California, USA; The Burnham Institute). PCT Int. Appl. WO 2000033076 A1 20000608, 95 pp. DESIGNATED STATES: W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US28591 19991201. PRIORITY: US 1998-PV110671 19981202; US 1998-PV113680 19981221; US 1998-PV114174 19981230.

AB This invention provides methods and kits for use in diagnosing genetically transmitted diseases that are assocd. with deficiencies in glycosylation of glycoconjugates such as glycoproteins, glycolipids, and proteoglycans. The methods and kits are also useful for monitoring the course of treatment of diseases that are assocd. with glycosylation disorders. Blood from patient with carbohydrate-deficient glycoprotein syndrome (CDGS) type II did not bind to E-PHA (erythroagglutinin of Phaseolus vulgaris) or to L-PHA (leucoagglutinin of Phaseolus vulgaris) lectins but showed increased binding to ConA lectin. Mouse models were constructed having defects in certain enzyme genes and the models were studied.

L14 ANSWER 4 OF 26 CAPLUS COPYRIGHT 2001 ACS
2000:178341 Document No. 132:306803 Molecular basis of variant pseudo-Hurler polydystrophy (mucolipidosis IIIC). Raas-Rothschild, Annick; Cormier-Daire, Valerie; Bao, Ming; Genin, Emmanuelle; Salomon, Remi; Brewer, Kevin; Zeigler, Marsha; Mandel, Hanna; Toth, Steve; Roe, Bruce; Munnich, Arnold; Canfield, William M. (Department of Human Genetics, Hadassah Hebrew University Hospital, Jerusalem, 91120, Israel). J. Clin. Invest., 105(5), 673-681 (English) 2000. CODEN: JCINAO. ISSN: 0021-9738. Publisher: American Society for Clinical Investigation.

AB Mucolipidosis IIIC (MLIIIC), or variant pseudo-Hurler polydystrophy, is an autosomal recessive disease of ***lysosomal*** ***hydrolase*** trafficking. Unlike the related diseases, mucolipidosis II and IIIA, the enzyme affected in mucolipidosis IIIC (N- ***Acetylglucosamine*** -1- ***phosphotransferase*** [GlcNAc- ***phosphotransferase***]) retains full transferase activity on synthetic substrates but lacks activity on ***lysosomal*** hydrolases. Bovine GlcNAc-phosphotransferase has recently been isolated as a multisubunit enzyme with the subunit structure .alpha.2.beta.2.gamma.2. We cloned the cDNA for the human .gamma.-subunit and localized its gene to chromosome 16p. We also showed, in a large multiplex Druze family that exhibits this disorder, that MLIIIC also maps to this chromosomal region. Sequence anal. of the .gamma.-subunit cDNA in patients from 3 families identified a frameshift mutation, in codon 167 of the .gamma. subunit, that segregated with the disease, indicating MLIIIC results from mutations in the phosphotransferase .gamma.-subunit gene. This is to our knowledge the first description of the mol. basis for a human mucolipidosis and suggests that the .gamma. subunit functions in ***lysosomal*** ***hydrolase*** recognition.

L14 ANSWER 5 OF 26 CAPLUS COPYRIGHT 2001 ACS
1996:614124 Document No. 126:116141 Effects of acute or chronic exposure to cold on the ***lysosomal*** enzyme system in rat tissues. Ohno, Hideki; Tanaka, Junji; Habara, Yoshiaki; Uehara, Yoshio; Kizaki, Takako; Oh-ishi, Shuji; Fukuda, Koichi; Gasa, Shinsei (Department Hygiene, National Defense Medical College, Tokorozawa, 359, Japan). Pathophysiology, 3(3), 181-185 (English) 1996. CODEN: PTHOE7. ISSN: 0928-4680. Publisher: Elsevier.

AB To investigate the effect of cold exposure on the ***lysosomal*** enzyme system in brown adipose tissue (BAT), liver, or kidney, 38 male Wistar rats were divided into the following four groups: (1) acute-cold-exposed rats at -5.degree.C for 1 h; (2) cold-acclimated rats at 5.degree.C for 4 wk; (3) cold-adapted rats by rearing at 5.degree.C for 40 successive generations; and (4) warm-acclimated rats at 25.degree.C (controls). The activities of the four ***lysosomal*** hydrolases measured (.beta.-glucuronidase, arylsulphatases A and B, and cathepsin D) in both BAT and liver from cold-acclimated and cold-adapted rats showed the same trends, namely, significant increases with one exception (.beta.-glucuronidase in cold-acclimated rats) as compared with warm-acclimated rats. The activity of N- ***acetylglucosamine*** -1- ***phosphotransferase*** , which generates a recognition marker for intracellular transport of the hydrolases to ***lysosomes*** via the Golgi app., increased significantly only in BAT from cold-acclimated rats, but decreased markedly, though unexpected, in liver from cold-adapted rats. On the other hand, the activity of N-acetylglucosamine phosphodiester .alpha.-N-acetylglucosamidase, which is another key enzyme for generation of the recognition marker, did not very substantially throughout the expts. Each exposure to cold appeared to rather reduce the activities of the ***lysosomal*** hydrolases in kidney. These results suggest that acute or chronic exposure to cold, in particular the latter, significantly affects the ***lysosomal*** enzyme system in rat BAT, liver, or kidney, and that the responses of each enzyme system are different from one another.

L14 ANSWER 6 OF 26 CAPLUS COPYRIGHT 2001 ACS
1995:620244 Document No. 123:50595 Purification and characterization of human serum N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase. Lee, Jin Kyu; Pierce, Michael (Complex Carbohydrate Res. Center, Univ. Georgia, Athens, GA, 30602, USA). Arch. Biochem. Biophys., 319(2), 413-25 (English) 1995. CODEN: ABBIA4. ISSN: 0003-9861.

AB Many lysosomal enzymes are recognized and selected by a unique marker in the form of mannose 6-phosphate groups which are present exclusively on their N-linked oligosaccharides. Two enzymes act sequentially to catalyze the addn. of mannose 6-phosphate groups to the proteins: N- ***acetylglucosamine*** ***phosphotransferase*** and

N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase (I). Here, the purifn. and partial characterization of I from human blood serum is reported. I was purified >600,000-fold by utilizing (NH4)2SO4 pptn., fractionation on wheat germ agglutinin-Sepharose, Fe3+-chelating Sepharose, and Cu2+-chelating Sepharose, and renaturation from gel slices after SDS-PAGE. I obsd. after renaturation and subsequent SDS-PAGE and Ag staining had an apparent mol. wt. of 118 kDa, which was slightly smaller than bovine liver I. Serum I activity did not require Triton X-100 and was not stimulated by its addn. These results suggest that I found in serum represents a form secreted after proteolysis in the Golgi app. of the membrane-bound enzyme. Serum I hydrolyzed UDP-GlcNAc to UDP and GlcNAc and hydrolyzed GlcNAc-P-Man.alpha.Me into .alpha.MeMan-P and GlcNAc. I had no hydrolytic activity toward UDP-GalNAc, UDP-Glc, [6-3H]GlcNAc.beta.1-3Gal.beta.1-4Glc, p-nitrophenyl-.alpha.-N-acetylglucosaminide, p-nitrophenyl-.beta.-N-acetylglucosamide, p-nitrophenyl-.alpha.-N-galactopyranoside, or p-nitrophenyl-.beta.-N-galactopyranoside. I was strongly inhibited by UDP-GlcNAc and GlcNAc-1-phosphate, had a pH optimum of 6.0-7.0, and was inhibited by FeCl3, FeSO4, and CuSO4. The Km values for UDP-GlcNAc and GlcNAc-P-Man.alpha.Me were 0.94 and 0.45 mM, resp. Over 77% of I activity remained after incubation for 10 min at 70.degree., demonstrating an unusual thermostability of the serum enzyme.

L14 ANSWER 7 OF 26 CAPLUS COPYRIGHT 2001 ACS
1995:376010 Document No. 123:4103 Lysosomal enzyme targeting. Purification and characterization of the two enzymes that catalyze the formation of mannose-6-phosphate from human lymphoblasts. Zhao, Ke-Wei (Univ. Calif., San Diego, CA, USA). 160 pp. Avail. Univ. Microfilms Int., Order No. DA9422574 From: Diss. Abstr. Int. B, 1994, 55(3), 743 (English) 1994.
AB Unavailable

L14 ANSWER 8 OF 26 CAPLUS COPYRIGHT 2001 ACS
1994:264244 Document No. 120:264244 Purification and kinetic parameters of bovine liver N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase. Mullis, Karen Gheesling; Huynh, Michiko; Kornfeld, Rosalind H. (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 269(3), 1718-26 (English) 1994. CODEN: JBCHA3. ISSN: 0021-9258.
AB The enzyme N-acetylglucosamine phosphodiester .alpha.-N-acetylglucosaminidase (phosphodiester .alpha.-GlcNAcase) catalyzes the second step in the formation of the mannose 6-phosphate targeting signal on lysosomal enzyme oligosaccharides by removing GlcNAc residues from GlcNAc-.alpha.-P-mannose moieties, which are formed in the first step by UDP-N- ***acetylglucosamine*** :glycoprotein N- ***acetylglucosamine*** -1- ***phosphotransferase*** (GlcNAc- ***phosphotransferase***). Phosphodiester .alpha.-GlcNAcase, a membrane-bound enzyme, has been purified about 3,000-fold from bovine liver to apparent homogeneity using detergent solubilization, fractionation on DEAE-cellulose, affinity chromatog. on lectin-Sepharose columns, gel filtration, and sodium dodecyl sulfate-polyacrylamide gel electrophoresis. The enzyme migrated as 129- and 121-kDa species on sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Since both bands had the same amino-terminal sequence, the smaller species is presumed to be derived from the larger by proteolysis. Kinetic anal. of bovine phosphodiester .alpha.-GlcNAcase with enzymically synthesized artificial and biol. substrates indicates that phosphodiester .alpha.-GlcNAcase requires GlcNAc-.alpha.-P R for substrate and that when R contains the Man.alpha.1,2Man linkage the substrate binding is most effective. Unlike GlcNAc-phosphotransferase, bovine phosphodiester .alpha.-GlcNAcase does not require a protein recognition determinant on lysosomal enzyme substrates.

L14 ANSWER 9 OF 26 CAPLUS COPYRIGHT 2001 ACS
1992:587145 Document No. 117:187145 ***Lysosomal*** enzyme phosphorylation. I. Protein recognition determinants in both lobes of procathepsin D mediate its interaction with UDP-GlcNAc: ***lysosomal*** enzyme N- ***acetylglucosamine*** -1- ***phosphotransferase*** . Baranski, Thomas J.; Cantor, Alan B.; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 267(32), 23342-8 (English) 1992. CODEN: JBCHA3. ISSN: 0021-9258.
AB The nature of a protein domain that is shared among ***lysosomal*** hydrolases and is recognized by the UDP-GlcNAc: ***lysosomal*** enzyme N-acetyl-glucosamine-1-phosphotransferase, the initial enzyme in the biosynthesis of mannose 6-phosphate residues, was investigated. Previously, elements of this recognition domain were identified using a chimeric protein approach. The combined substitution of two regions

(amino acids 188-230, particularly lysine 203, and 265-292) from the carboxyl lobe of the ***lysosomal*** ***hydrolase*** cathepsin D into the homologous positions of the related secretory protein glycopepsinogen was sufficient to confer recognition by phosphotransferase and subsequent phosphorylation of the oligosaccharides when this chimeric protein was expressed in Xenopus oocytes. (Baranski, T. J., et al., 1990). The current study demonstrates that when these two regions are replaced in cathepsin D by the homologous glycopepsinogen amino acids, the resultant chimeric mol. is poorly phosphorylated. However, when either of these regions is substituted individually, the chimeric mols. are well phosphorylated. The phosphorylation of these latter chimeric proteins is dependent on the presence of procathepsin D amino lobe elements. By analyzing a series of chimeric proteins that contain all eight combinations of three consecutive segments of the entire amino lobe of procathepsin D, it was found that multiple regions of the amino lobe of cathepsin D enhance phosphorylation of the chimeric proteins. These elements may be part of an extended carboxyl lobe recognition domain or comprise a second independent recognition domain.

L14 ANSWER 10 OF 26 CAPLUS COPYRIGHT 2001 ACS

1991:653020 Document No. 115:253020 Elevated carbohydrate phosphotransferase activity in human hepatoma and phosphorylation of cathepsin D. Ohhira, M.; Gasa, S.; Makita, A.; Sekiya, C.; Namiki, M. (Sch. Med., Hokkaido Univ., Sapporo, 060, Japan). Br. J. Cancer, 63(6), 905-8 (English) 1991. CODEN: BJCAAI. ISSN: 0007-0920.

AB To det. the cause of the increased content of carbohydrate-bound phosphate in tumor lysosomal hydrolases, the activity and kinetics in human hepatocellular carcinoma of two enzymes involved in the formation of mannose-6-phosphate in lysosomal hydrolases UDP-GlcNAc: lysosomal enzyme GlcNAc.alpha. 1-phosphotransferase (GlcNAc-phosphotransferase) and phosphodiester glycosidase were studied. The activity level of the phosphotransferase with artificial and natural substrates was elevated in hepatoma compared to that in uninvolved tissue, while the phosphodiester glycosidase of hepatoma was at a level similar to that of the uninvolved tissue. To verify a previous observation that cathepsin D of human hepatoma contained increased GlcNAc-phosphomannose, the protease was examd. for carbohydrate phosphorylation by the GlcNAc-phosphotransferase. The protease from normal human liver was much more phosphorylated than hepatoma protease, confirming the previous observation. The predominant phosphorylation of the protease occurred in one of two major heavy subunits, with some phosphorylation in one of two minor light subunits.

L14 ANSWER 11 OF 26 CAPLUS COPYRIGHT 2001 ACS

1991:627034 Document No. 115:227034 Mapping and molecular modeling of a recognition domain for ***lysosomal*** enzyme targeting. Baranski, Thomas J.; Koelsch, Gerald; Hartsuck, Jean A.; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 266(34), 23365-72 (English) 1991. CODEN: JBCHA3. ISSN: 0021-9258.

AB ***Lysosomal*** enzymes contain a common protein determinant that is recognized by UDP-GlcNAc: ***lysosomal*** enzyme N-***acetylglucosamine*** -1- ***phosphotransferase*** , the initial enzyme in the biosynthesis of mannose-6-phosphate residues. Previously, a ***lysosomal*** enzyme recognition domain was generated by substituting two regions (lysine 203 and amino acids 265-292) of the ***lysosomal*** ***hydrolase*** cathepsin D into a related secretory protein glycopepsinogen. When expressed in Xenopus oocytes, the oligosaccharides of the chimeric protein were efficiently phosphorylated (Baranski, T. J. et al., 1990). In the current study, incremental substitutions of cathepsin D residues into glycopepsinogen and alanine-scanning mutagenesis were utilized to define the recognition domain more precisely. A computer-generated model of the cathepsin D/pepsinogen chimeric mol. served as a guide for mutagenesis and for the interpretation of results. These studies indicate that the recognition domain is a surface patch that contains multiple interacting sites. There is a strict positional requirement for the lysine residue at position 203.

L14 ANSWER 12 OF 26 CAPLUS COPYRIGHT 2001 ACS

1991:245207 Document No. 114:245207 Carbohydrate phosphotransferase in human hepatoma and phosphorylation of cathepsin D. Ohhira, Motoyuki (Sch. Med., Hokkaido Univ., Sapporo, 060, Japan). Hokkaido Igaku Zasshi, 65(6), 560-7 (Japanese) 1990. CODEN: HOIZAK. ISSN: 0367-6102.

AB N- ***Acetylglucosamine*** -1- ***phosphotransferase*** (I) and phosphodiester glycosidase (II) involved in formation of mannose-6-phosphate in lysosomal hydrolases were studied for the activity and kinetics in human hepatocellular carcinoma. The activity level of I

with an artificial substrate was elevated in hepatoma as compared with that in normal liver, whereas II of hepatoma was at control level. The elevation was more remarkable with the physiol. substrate cathepsin D. The liver protease was much more phosphorylated by I than the hepatoma protease. The predominant phosphorylation of the protease occurred in the heavy subunit (31 kDa).

L14 ANSWER 13 OF 26 CAPLUS COPYRIGHT 2001 ACS
1990:627089 Document No. 113:227089 Generation of a ***lysosomal*** enzyme targeting signal in the secretory protein pepsinogen. Baranski, Thomas J.; Faust, Phyllis L.; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). Cell (Cambridge, Mass.), 63(2), 281-91 (English) 1990. CODEN: CELLB5. ISSN: 0092-8674.
AB ***Lysosomal*** enzymes contain a common protein determinant that is recognized by ***lysosomal*** enzyme N- ***acetylglucosamine*** -1- ***phosphotransferase*** , the initial enzyme in the formation of mannose 6-phosphate residues. To identify this protein determinant, chimeric mols. between 2 aspartyl proteases, cathepsin D, a ***lysosomal*** enzyme, and pepsinogen, a secretory protein, were constructed. When expressed in Xenopus oocytes, the oligosaccharides of cathepsin D were efficiently phosphorylated, whereas the oligosaccharides of a glycosylated form of pepsinogen were not phosphorylated. The combined substitution of 2 noncontinuous sequences of cathepsin D (lysine-203 and amino acids 265-292) into the analogous positions of glycopepsinogen resulted in phosphorylation of the oligosaccharides of the expressed chimeric mol. These 2 sequences were in direct apposition on the surface of the mol., indicating that amino acids from different regions come together in 3-dimensional space to form this recognition domain. Other regions of cathepsin D were identified that may be components of a more extensive recognition marker.

L14 ANSWER 14 OF 26 CAPLUS COPYRIGHT 2001 ACS
1989:475564 Document No. 111:75564 Processing enzymes acting on carbohydrate moiety of lysosomal hydrolases in leukemic cells: elevated activity of N- ***acetylglucosamine*** -1- ***phosphotransferase*** . Uehara, Yoshio; Gasa, Shinsei; Makita, Akira; Oh-hira, Motoyuki; Sakurada, Keisuke; Miyazaki, Tamotsu (Sch. Med., Hokkaido Univ., Sapporo, 060, Japan). Blood, 73(7), 1957-62 (English) 1989. CODEN: BLOOAW. ISSN: 0006-4971.
AB It was previously demonstrated that an acidic variant form of lysosomal arylsulfatase B which accumulates in chronic myelogenous leukemia (CML) cells is highly phosphorylated at its carbohydrate moiety. Since lysosomal hydrolases including the sulfatase underwent the posttranslational phosphorylation processing at the carbohydrate moiety, two enzymes acting in the processing were investigated in peripheral leukocytes from leukemia patients. The activity level of the first enzyme in the processing, an N- ***acetylglucosamine*** -1- ***phosphotransferase*** which forms a phosphodiester at the carbohydrates, was significantly higher in CML cells than in normal control cells. The transferase level in CML cells was also higher compared with that in normal bone marrow cells, which include myeloid progenitor cells. However, the activity of the second processing enzyme, a phosphodiester glycosidase that converts a phosphodiester to a phosphomonoester, showed no consistent change in CML cells. Thus, the increment in the sulfatase variant contg. phosphomonoesters and diesters in CML cells is most probably assocd. with elevated activities of the phosphotransferase. In two cases of CML in blast crisis and a case of acute myelogenous leukemia (AML), activity of the processing enzyme was considerably decreased concomitant with redn. of peripheral blastic cells by chemotherapy.

L14 ANSWER 15 OF 26 CAPLUS COPYRIGHT 2001 ACS
1988:568369 Document No. 109:168369 Biochemical studies on lymphoblastoid cells with inherited N-acetyl-glucosamine 1-phosphotransferase deficiency (I-cell disease). Okada, Shintaro; Handa, Masafumi; Hashimoto, Tomoko; Nishimoto, Junji; Inui, Koji; Furukawa, Masumi; Furuyama, Junichi; Yabuuchi, Hyakuji; Tate, Mutsuko; et al. (Dep. Pediatr., Osaka Univ. Hosp., Osaka, 553, Japan). Biochem. Int., 17(2), 375-83 (English) 1988. CODEN: BIINDF. ISSN: 0158-5231.
AB Lymphoblastoid cells transformed by Epstein-Barr virus from peripheral lymphocytes of normal individuals and I-cell disease (ICD) patients were used for the enzymic study of ***lysosomal*** hydrolases and N- ***acetylglucosamine*** 1- ***phosphotransferase*** . ICD lymphoblastoid cells secreted a larger amt. of hydrolases into medium than normal cells, although the intracellular hydrolases were not deficient in ICD cells. The stimulating effect of 10 mM ammonium chloride on secretion

of hydrolases was found only with normal cells, and not with ICD cells, indicating that the ***hydrolase*** mol. bearing mannose 6-phosphate was secreted. The ICD lymphoblastoid cells retained the enzymol. characteristics of both ***lysosomal*** hydrolases and N-***acetylglucosamine*** 1- ***phosphotransferase*** seen in ICD fibroblasts, which enables the study the pathophysiol. of ICD in cells other than fibroblasts.

L14 ANSWER 16 OF 26 CAPLUS COPYRIGHT 2001 ACS
1988:404631 Document No. 109:4631 UDP-N-acetylglucosamine: ***lysosomal*** enzyme precursor N-acetylglucosamine-1-phosphate transferase activities in human ovarian tumor tissue and some transformed cell lines. Madiyalakan, Ragupathy; Mueller, O. Thomas; Shows, Thomas B.; Matta, Khushi L. (Roswell Park Mem. Inst., New York State Dep. Health, Buffalo, NY, 14263, USA). Cancer Invest., 5(6), 553-8 (English) 1987. CODEN: CINVD7. ISSN: 0735-7907.
AB UDP-N-acetylglucosamine: ***lysosomal*** enzyme precursor N-acetyl-glucosamine-1-phosphate transferase, is a key enzyme involved in the intracellular targeting of ***lysosomal*** enzymes. This enzyme was elevated 4-fold in primary ovarian tumor microsomes with respect to normal ovarian microsomes. This elevation was assocd. with increases in the specific activity of multiple ***lysosomal*** hydrolases, including .beta.-D-hexosaminidase, .alpha.-L-fucosidase, and .beta.-D-galactosidase. The activity of the phosphotransferase was also documented in several cell lines derived from human tumors. The possible role of this enzyme in tumor-assocd. phosphorylation is discussed.

L14 ANSWER 17 OF 26 CAPLUS COPYRIGHT 2001 ACS
1987:29331 Document No. 106:29331 Involvement of cis and trans Golgi apparatus elements in the intracellular sorting and targeting of acid hydrolases to ***lysosomes*** . Minnifield, Nita; Creek, Kim E.; Navas, Placido; Morre, D. James (Dep. Biol. Sci., Purdue Univ., West Lafayette, IN, USA). Eur. J. Cell Biol., 42(1), 92-100 (English) 1986. CODEN: EJCBDN. ISSN: 0171-9335.
AB To delineate the traffic route through the Golgi app. followed by newly synthesized ***lysosomal*** enzymes, the Golgi app. of rat liver was subfractionated by preparative free-flow electrophoresis into cisternae fractions of increasing content of trans face markers and decreasing contents of markers for the cis face. NADPase was used to mark median cisternae. .beta.-Hexosaminidase, the high-mannose oligosaccharide-processing enzyme, .alpha.-mannosidase II, the 2 enzymes involved in the biosynthesis of the phosphomannosyl recognition marker, and the phosphomannosyl receptor itself decreased in specific activity or amt. from cis to trans. Addnl., these activities were obsd. in a fraction consisting predominantly of cisternae, vesicles and tubules derived from trans-most Golgi app. elements. These results, along with preliminary pulse-labeling kinetic data for the phosphomannosyl receptor, suggest that ***lysosomal*** enzymes enter the Golgi app. at the cis face, are phosphorylated, and appear in trans face vesicles by a route whereby the phosphomannosyl receptor bypasses at least some median and(or) trans Golgi app. cisternae.

L14 ANSWER 18 OF 26 CAPLUS COPYRIGHT 2001 ACS
1986:402552 Document No. 105:2552 Molecular size of N-acetylglucosaminylphosphotransferase and .alpha.-N-acetylglucosaminyl phosphodiesterase as determined in situ in Golgi membranes by radiation inactivation. Ben-Yoseph, Yoav; Potier, Michel; Pack, Beverley A.; Mitchell, Deborah A.; Melancon, Serge B.; Nadler, Henry L. (Sch. Med., Wayne State Univ., Detroit, MI, 48201, USA). Biochem. J., 235(3), 883-6 (English) 1986. CODEN: BIJOAK. ISSN: 0306-3275.
AB The radiation inactivation method was used to det. the mol. size of the 2 enzymes that participate in the synthesis of the phosphomannosyl recognition marker of lysosomal proteins. The detns. were carried out in situ, in Golgi membranes isolated from normal human placenta and cultured skin fibroblasts. A mol. size of 228 kilodaltons (kDa) was found for placental N-acetylglucosaminylphosphotransferase, and 129 kDa for placental .alpha.-N-acetylglucosaminyl phosphodiesterase. The values for the fibroblast enzymes were .apprx.20% higher, 283 and 156 kDa for the transferase and phosphodiesterase, resp. Triton X-100 had no effect on the mol. size of these enzymes.

L14 ANSWER 19 OF 26 CAPLUS COPYRIGHT 2001 ACS
1985:594441 Document No. 103:194441 Heterogeneity in I-cell disease (mucolipidosis II). Okada, Shintaro; Kato, Tomochika; Yutaka, Tohru; Midorikawa, Mitsuo; Dohke, Mariko; Ohshima, Toshio; Yabuuchi, Hyakuji

(Dep. Pediatr., Osaka Univ. Hosp., Osaka, Japan). Dev. Brain Its Disord., Proc. Int. Symp. Dev. Disabil., 4th, Meeting Date 1983, 151-9. Editor(s): Arima, Masataka; Suzuki, Yoshiyuki; Yabuuchi, Hyakuji. Karger: Basel, Switz. (English) 1985. CODEN: 53XKAR.

AB When fibroblasts from humans with I-cell disease (ICD) were cultured with sucrose, the activities of intracellular ***lysosomal*** hydrolases increased to normal fibroblast levels in 3 of 8 cases studied. In the other 5 cases, the hydrolases did not respond to sucrose treatment. The hydrolases that were normalized included .beta.-galactosidase, .beta.-hexosaminidase, .alpha.-mannosidase, and .alpha.-fucosidase. Thus, the authors propose that ICD be classified into 2 subgroups. The mechanism which allows for this activation of hydrolases in some patients is discussed in relation to the stimulation of UDP-N-***acetylglucosamine*** :glycoprotein N-acetyl glucosaminyl ***phosphotransferase*** and the normalization of oligosaccharide structure of ***lysosomal*** ***hydrolase*** mols.

L14 ANSWER 20 OF 26 CAPLUS COPYRIGHT 2001 ACS

1984:625368 Document No. 101:225368 Radiometric assays of N-acetylglucosaminylphosphotransferase and .alpha.-N-acetylglucosaminyl phosphodiesterase with substrates labeled in the glucosamine moiety. Ben-Yoseph, Yoav; Baylerian, Michael S.; Nadler, Henry L. (Sch. Med., Wayne State Univ., Detroit, MI, 48201, USA). Anal. Biochem., 142(2), 297-304 (English) 1984. CODEN: ANBCA2. ISSN: 0003-2697.

AB The assay of fibroblast and leukocyte N-acetylglucosaminylphosphotransfera se with .alpha.-methylmannoside acceptor and com. available UDP-N-[3H or 14C]acetylglucosamine donor was modified to yield low background and consequently high sensitivity and reliability comparable to those obtained with the synthetically made [.beta.-32P]UDP-N-acetylglucosamine donor. This was achieved by an addnl. elution step that removed free N-[3H or 14C] acetylglucosamine which appeared to be the breakdown product responsible for the high background. In addn., the N-[3H or 14C]acetylglucosamine-1-phospho-6-.alpha.-methylmannoside product of the transfer reaction was then isolated and, following desalting, could serve as a substrate for the assay of .alpha.-N-acetylglucosaminyl phosphodiesterase. Cell prepns. of patients with I-cell disease and pseudo-Hurler polydystrophy demonstrated severe to moderate deficiency of transferase activity and normal phosphodiesterase activity toward the resp. substrates labeled with 3H or 14C in the glucosamine moiety.

L14 ANSWER 21 OF 26 CAPLUS COPYRIGHT 2001 ACS

1984:170670 Document No. 100:170670 Studies of the synthesis, structure and function of the phosphorylated oligosaccharides of lysosomal enzymes. Varki, Ajit P.; Reitman, Marc L.; Tabas, Ira; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63130, USA). J. Biosci., 5(Suppl. 1), 101-4 (English) 1983. CODEN: JOBSDN.

AB The synthesis, structure, and function of the phosphorylated oligosaccharides of lysosomal enzymes, esp. .beta.-glucuronidase of mouse lymphoma cells, are discussed. The role of the sequential action of N-***acetylglucosamine*** 1- ***phosphotransferase*** and .alpha.-N-acetylglucosaminyl phopshodiesterase in the phosphorylation of the mannose residues of the oligosaccharides is shown. The human syndromes of I-cell disease and pseudo-Hurler polydystrophy are caused by deficiencies of the N- ***acetylglucosamine*** 1-***phosphotransferase*** .

L14 ANSWER 22 OF 26 CAPLUS COPYRIGHT 2001 ACS

1983:450859 Document No. 99:50859 Subfractionation of rat liver Golgi apparatus: Separation of enzyme activities involved in the biosynthesis of the phosphomannosyl recognition marker in lysosomal enzymes. Deutscher, Susan L.; Creek, Kim E.; Merion, Michael; Hirschberg, Carlos B. (Sch. Med., St. Louis Univ., St. Louis, MO, 63104, USA). Proc. Natl. Acad. Sci. U. S. A., 80(13), 3938-42 (English) 1983. CODEN: PNASA6. ISSN: 0027-8424.

AB A highly purified Golgi app. prepn. from rat liver was subfractionated on a Percoll gradient into 2 major protein peaks of similar size that migrated at densities of 1.028 and 1.051 g/mL. The lighter protein peak contained 70-80% of the total activities of the oligosaccharide-processing enzymes .alpha.-1,2-mannosidase and mannosidase II and of .alpha.-N-acetylglucosaminylphosphotransferase, an enzyme involved in the biosynthesis of the mannose 6-phosphate recognition marker of lysosomal enzymes. The enzymes activities were enriched 2-fold in specific activity over that of the heavy protein peak. In contrast, 80% of the .alpha.-N-acetylglucosaminylphosphodiesterase, an enzyme that exposes 6-phosphomonoesters of mannose on the oligosaccharide chains of lysosomal

enzymes, migrated in a region of slightly higher d. than did the protein peak of d. 1.051 g/mL. Sialyltransferase and galactosyltransferase activities distributed almost equally among the 2 protein peaks. Controls ruled out that the 2 protein peaks were the result of aggregation/deaggregation and that enzyme activities were altered by Percoll per se. Lysosomal enzyme activities migrated in a region essentially devoid of Golgi app.-assocd. enzyme activities. Apparently, a phys. sepn. exists within the Golgi app. of some of the enzymes involved in the biosynthesis and processing of the oligosaccharides on glycoproteins, including those responsible for the formation of the mannose 6-phosphate recognition marker on lysosomal enzymes.

L14 ANSWER 23 OF 26 CAPLUS COPYRIGHT 2001 ACS
1983:158284 Document No. 98:158284 Evidence for extensive subcellular organization of asparagine-linked oligosaccharide processing and lysosomal enzyme phosphorylation. Goldberg, Daniel E.; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 258(5), 3159-65 (English) 1983. CODEN: JBCHA3. ISSN: 0021-9258.
AB Membranes prepd. from mouse lymphoma BW5147.3 cells and P388D1 macrophages were fractionated on a continuous sucrose gradient and assayed for enzymes involved in the processing of asparagine-linked oligosaccharides. The order in which these enzymes distributed from dense to light membranes correlated with the established sequence of events in glycoprotein biosynthesis. A no. of enzymes which have been previously localized to the Golgi sepd. into 4 regions on the gradient. UDP-N-acetylglucosamine:lysosomal enzyme N- ***acetylglucosamine*** -1- ***phosphotransferase*** , the enzyme which catalyzes the selective phosphorylation of the high mannose oligosaccharides of lysosomal enzymes, was present in the densest membranes. N-Acetylglucosamine 1-phosphodiester .alpha.-N-acetylglucosaminidase was in the next region. Several enzymes involved in the late stages of asparagine-linked oligosaccharide processing were localized to the 3rd region. UDP-galactose:N-acetylglucosamine galactosyltransferase was present in the lightest membranes (region IV). Pulse-chase expts. utilizing [2-3H]mannose demonstrated that the distribution of in vivo labeled asparagine-linked oligosaccharide intermediates correlates with the distribution of these processing enzymes. Anal. of the phosphorylated oligosaccharides of lysosomal enzymes which were bound to the phosphomannosyl receptor indicated that these enzymes had already passed through the region of the Golgi which contains galactosyltransferase and sialyltransferase. These findings are consistent with there being a high degree of organization within the Golgi complex. The phys. sepn. of processing enzymes could serve as one mechanism for the control of asparagine-linked oligosaccharide biosynthesis.

L14 ANSWER 24 OF 26 CAPLUS COPYRIGHT 2001 ACS
1983:67540 Document No. 98:67540 Steps in the phosphorylation of the high mannose oligosaccharides of ***lysosomal*** enzymes. Kornfeld, Stuart; Reitman, Marc L.; Varki, Ajit; Goldberg, Daniel; Gabel, Christopher A. (Sch. Med., Washington Univ., St Louis, MO, 63110, USA). Ciba Found. Symp., 92(Membr. Recycl.), 138-56 (English) 1982. CODEN: CIBSB4. ISSN: 0300-5208.
AB A review with 35 refs. on the phosphorylation path of ***lysosomal*** acid hydrolases by N- ***acetylglucosamine*** 1- ***phosphotransferase*** and .alpha.-N- ***acetylglucosamine*** ***phosphodiesterase*** .

L14 ANSWER 25 OF 26 CAPLUS COPYRIGHT 2001 ACS
1982:435344 Document No. 97:35344 Synthesis of phosphorylated recognition marker in lysosomal enzymes is located in the cis part of Golgi apparatus. Pohlmann, Regina; Waheed, Abdul; Hasilik, Andrej; Von Figura, Kurt (Physiol. Chem. Inst., Univ. Muenster, Muenster, D 4400, Fed. Rep. Ger.). J. Biol. Chem., 257(10), 5323-5 (English) 1982. CODEN: JBCHA3. ISSN: 0021-9258.
AB Rat liver membranes were subjected to centrifugation in a sucrose d. gradient in which the Golgi app. was sepd. into several subfractions. Two enzymes involved in the synthesis of the phosphorylated recognition marker in lysosomal enzymes, UDP-N-acetylglucosamine-lysosomal enzyme precursor N- ***acetylglucosamine*** -1- ***phosphotransferase*** and .alpha.-N-acetylglucosaminyl phosphodiesterase, fractionated with .alpha.-1,2-mannosidase, a marker enzyme of cis Golgi membranes, and differentially from galactosyltransferase, a marker enzyme of trans Golgi membranes.

L14 ANSWER 26 OF 26 CAPLUS COPYRIGHT 2001 ACS

1981:421780 Document No. 95:21780 Subcellular location of two enzymes involved in the synthesis of phosphorylated recognition markers in lysosomal enzymes. Waheed, Abdul; Pohlmann, Regina; Hasilik, Andrej; Von Figura, Kurt (Inst. Physiol. Chem., Univ. Muenster, Muenster, D 4400, Fed. Rep. Ger.). J. Biol. Chem., 256(9), 4150-2 (English) 1981. CODEN: JBCHA3. ISSN: 0021-9258.

AB Phosphorylated recognition markers in lysosomal enzymes appear to be synthesized by transfer of .alpha.-N-acetylglucosamine 1-phosphate groups to the C6 hydroxyl group of mannose residues in glycosylated enzyme precursors and a subsequent hydrolysis from the diester groups of the N-acetylglucosamine residues. The UDP- ***acetylglucosamine*** -glycoprotein ***acetylglucosamine*** -1- ***phosphotransferase*** and acetylglucosaminyl phosphodiesterase activities were studied in subcellular fractions of rat liver. Both activities fractionated in a similar manner to the Golgi marker, UDP-galactose-glycoprotein galactosyltransferase.

=> E CANFIELD W/AU
=> S E8-E10

	2	"CANFIELD WILLIAM"/AU
	17	"CANFIELD WILLIAM M"/AU
	1	"CANFIELD WILLIAM MONROE"/AU
L15	20	("CANFIELD WILLIAM"/AU OR "CANFIELD WILLIAM M"/AU OR "CANFIELD WILLIAM MONROE"/AU)

=> S L15 NOT L14

L16 18 L15 NOT L14

=> D 2,4,7,8,10-12 CBIB ABS

L16 ANSWER 2 OF 18 CAPLUS COPYRIGHT 2001 ACS

1999:738356 Document No. 132:60839 Molecular cloning and functional expression of two splice forms of human N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase. Kornfeld, Rosalind; Bao, Ming; Brewer, Kevin; Noll, Carolyn; ***Canfield, William*** (Department of Medicine, Washington University School of Medicine, St. Louis, MO, 63110, USA). J. Biol. Chem., 274(46), 32778-32785 (English) 1999. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular Biology.

AB We have isolated and sequenced human cDNA and mouse genomic DNA clones encoding N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase (phosphodiester .alpha.-GlcNAcase) which catalyzes the second step in the synthesis of the mannose 6-phosphate recognition signal on lysosomal enzymes. The gene is organized into 10 exons. The protein sequence encoded by the clones shows 80% identity between human and mouse phosphodiester .alpha.-GlcNAcase and no homol. to other known proteins. It predicts a type I membrane-spanning glycoprotein of 514 amino acids contg. a 24-amino acid signal sequence, a luminal domain of 422 residues with six potential N-linked glycosylation sites, a single 27-residue transmembrane region, and a 41-residue cytoplasmic tail that contains both a tyrosine-based and an NPF internalization motif. Human brain expressed sequence tags lack a 102-base pair region present in human liver cDNA that corresponds to exon 8 in the genomic DNA and probably arises via alternative splicing. COS cells transfected with the human cDNA expressed 50-100-fold increases in phosphodiester .alpha.-GlcNAcase activity proving that the cDNA encodes the subunits of the tetrameric enzyme. Transfection with cDNA lacking the 102-base pair region also gave active enzyme. The complete genomic sequence of human phosphodiester .alpha.-GlcNAcase was recently deposited in the data base. It showed that our cDNA clone was missing only the 5'-untranslated region and initiator methionine and revealed that the human genomic DNA has the same exon organization as the mouse gene.

L16 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2001 ACS

1998:592720 Document No. 129:299526 Purification and multimeric structure of bovine N-acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase. Kornfeld, Rosalind; Bao, Ming; Brewer, Kevin; Noll, Carolyn; ***Canfield, William M.*** (Department of Medicine, Washington University School of Medicine, St. Louis, MO, 63110, USA). J. Biol. Chem., 273(36), 23203-23210 (English) 1998. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular

Biology.

AB N-Acetylglucosamine-1-phosphodiester .alpha.-N-acetylglucosaminidase (EC 3.1.4.45; phosphodiester .alpha.-GlcNAcase) catalyzes the second step in the synthesis of the mannose 6-phosphate determinant required for efficient intracellular targeting of newly synthesized lysosomal hydrolases to the lysosome. A partially purified prepn. of phosphodiester .alpha.-GlcNAcase from bovine pancreas was used to generate a panel of murine monoclonal antibodies. The anti-phosphodiester .alpha.-GlcNAcase monoclonal antibody UC1 was coupled to a solid support and used to immunopurify the bovine liver enzyme 670,000-fold in 2 steps to apparent homogeneity with an overall yield of 14%. The purified phosphodiester .alpha.-GlcNAcase has a specific activity of 498 .mu.mol of [3H]GlcNAc-.alpha.-phosphomannose-.alpha.-Me cleaved per h per mg of protein using 0.5 mM [3H]GlcNAc-.alpha.-phosphomannose-.alpha.-Me as substrate. The subunit structure of the enzyme was detd. using a combination of anal. gel filtration chromatog., SDS-PAGE, and N-terminal sequencing. The data indicate that bovine phosphodiester .alpha.-GlcNAcase is a 272,000-Da complex of 4 identical 68,000-Da glycoprotein subunits arranged as 2 disulfide-linked homodimers. A sol. form of the enzyme, isolated from fetal bovine serum, showed the same subunit structure. Both forms of the enzyme reacted with a rabbit antibody raised to the N-terminal peptide of the liver enzyme, suggesting that phosphodiester .alpha.-GlcNAcase is a type I membrane-spanning glycoprotein with its N-terminus in the lumen of the Golgi app.

L16 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2001 ACS

1996:762181 Document No. 126:44245 Bovine UDP-N-acetylglucosamine:lysosomal-enzyme N-acetylglucosamine-1-phosphotransferase. II. Enzymic characterization and identification of the catalytic subunit. Bao, Ming; Elmendorf, B. Jean; Booth, J. Leland; Drake, Richard R.; ***Canfield,*** *** William M.*** (W. K. Warren Med. Res. Inst., Univ. Oklahoma Health Sci. Cent., Oklahoma City, OK, 73104, USA). J. Biol. Chem., 271(49), 31446-31451 (English) 1996. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular Biology.

AB The kinetic properties of lysosomal enzyme N-acetylglucosamine-1-phosphotransferase (I) purified to homogeneity from lactating bovine mammary gland were investigated. I transferred GlcNAc 1-phosphate from UDP-GlcNAc to the synthetic acceptor, .alpha.-methylmannoside, generating GlcNAc-1-phospho-6-mannose .alpha.-Me, the structure of which was confirmed by mass spectroscopy. I was active at pH 5.7-9.3, with optimal activity at pH 6.6-7.5. I activity was strictly dependent on Mg2+ or Mn2+. The Km for Mn2+ was 185 .mu.M. The Km values for UDP-GlcNAc and .alpha.-methylmannoside were 30 .mu.M and 63 mM, resp. I was competitively inhibited by UDP-Glc, with a Ki of 733 .mu.M. The 166-kDa subunit was identified as the catalytic subunit by photoaffinity labeling with azido-[.beta.-32P]UDP-Glc. Purified I utilized the lysosomal enzyme, uteroferrin, .apprx.163-fold more effectively than the nonlysosomal glycoprotein, RNase B. Antibodies to I blocked transfer to cathepsin D, but not to .alpha.-methylmannoside, suggesting that protein-protein interactions are required for the efficient utilization of glycoprotein acceptors. These results indicate that the purified bovine I retains the specificity for lysosomal enzymes as acceptors previously obsd. with crude prepns.

L16 ANSWER 8 OF 18 CAPLUS COPYRIGHT 2001 ACS

1996:762180 Document No. 126:100959 Bovine UDP-N-acetylglucosamine:lysosomal-enzyme N-acetylglucosamine-1-phosphotransferase. I. Purification and subunit structure. Bao, Ming; Booth, J. Leland; Elmendorf, B. Jean; ***Canfield, William M.*** (W. K. Warren Med. Res. Inst., Univ. Oklahoma Health Sci. Cent., Oklahoma City, OK, 73104, USA). J. Biol. Chem., 271(49), 31437-31445 (English) 1996. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular Biology.

AB Lysosomal enzyme N-acetylglucosamine-1-phosphotransferase (I) catalyzes the initial step in the synthesis of the mannose 6-phosphate determinant required for efficient intracellular targeting of newly synthesized lysosomal hydrolases to the lysosome. I was partially purified .apprx.30,000-fold by chromatog. of solubilized membrane proteins from lactating bovine mammary glands on DEAE-Sepharose, Reactive Green 19-agarose, and Superose 6. Partially purified I was used to generate a panel of murine monoclonal antibodies. Anti-I monoclonal antibody PT18 was coupled to a solid support and used to immunopurify I .apprx.480,000-fold to apparent homogeneity with an overall yield of 29%. Purified I had a specific activity of 10-12 .mu.mol N-acetylglucosamine-1-phosphate transferred/h/mg protein using 100 mM .alpha.-methylmannoside as acceptor. The subunit structure of I was detd. using a combination of

anal. gel filtration chromatog., SDS-PAGE, and N-terminal sequencing. The results indicated that bovine I is a 540 kDa complex composed of disulfide-linked homodimers of 166- and 51-kDa subunits and 2 identical, noncovalently assocd. 56-kDa subunits.

L16 ANSWER 10 OF 18 CAPLUS COPYRIGHT 2001 ACS
1992:440663 Document No. 117:40663 Characterization of the signal for rapid internalization of the bovine mannose 6-phosphate/insulin-like growth factor-II receptor. Jadot, Michel; ***Canfield, William M.*** ; Gregory, Walter; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 267(16), 11069-77 (English) 1992. CODEN: JBCHA3. ISSN: 0021-9258.
AB The signal for rapid internalization of the mannose 6-phosphate/insulin-like growth factor II receptor has been localized to the sequence Tyr-Lys-Tyr-Ser-Lys-Val in positions 24-29 of its 163-residue cytoplasmic tail. Most of the activity of this signal is mediated by the carboxyl 4 amino acids, esp. Tyr26 and Val29 (Canfield, W. M., Johnson, K. F., Ye, R. D., Gregory, W. and Kornfeld, S. (1991) J. Biol. Chem. 266, 5682-5688). In this study, the effect of a series of mutations on the internalization rate of a mutant receptor that contains a 29-amino acid cytoplasmic tail terminating with the 4-amino acid internalization sequence Tyr-Ser-Lys-Val was tested. Replacement of Tyr26 with Phe or Trp gave rise to mutant receptors that were internalized at 10% the wild-type rate, whereas receptors with Ala, Leu, Ile, Val, or Asn at this position were totally inactive. Val29 could be replaced by other large hydrophobic residues (Phe, Leu, Ile, or Met) with no loss of activity, but the presence of Ala, Gly, Arg, Gln, or Tyr in this position inactivated the signal. Ser27 could be effectively replaced by many different amino acids, but not by Pro or Gly. However, Gly27 could be tolerated if the residues at positions 28 and 29 were also changed. A change in the 2-residue spacing between Tyr26 and Val29 destroyed the signal. These data show that the essential elements of this signal are an arom. residue, esp. a Tyr, in the first position, sepd. from a large hydrophobic residue in the last position by 2 amino acids. The residues in positions 2 and 3 of the signal may have a modulating effect on its activity. The Tyr-Ser-Lys-Val signal could be moved to a more proximal region of the cytoplasmic tail with only a modest loss of activity. In addn., the signal could be effectively replaced by the putative 4-residue signals of 7 other receptors and membrane proteins known to undergo rapid endocytosis, including the Tyr-Thr-Arg-Phe sequence of the transferrin receptor, a Type II membrane protein. These results are compatible with the 4-residue signals of this type being interchangeable, even among Type I and Type II membrane proteins.

L16 ANSWER 11 OF 18 CAPLUS COPYRIGHT 2001 ACS
1991:405831 Document No. 115:5831 Localization of the signal for rapid internalization of the bovine cation-independent mannose 6-phosphate/insulin-like growth factor-II receptor to amino acids 24-29 of the cytoplasmic tail. ***Canfield, William M.*** ; Johnson, Karl F.; Ye, Richard D.; Gregory, Walter; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 266(9), 5682-8 (English) 1991. CODEN: JBCHA3. ISSN: 0021-9258.
AB The signal for the rapid internalization of the cation-independent mannose 6-phosphate/insulin-like growth factor-II receptor has been previously localized to the inner half of the 163-amino acid cytoplasmic tail, including tyrosine 24 and tyrosine 26. To define this signal more precisely, a series of truncation and substitution mutants were generated and analyzed for their ability to mediate the endocytosis of extracellular lysosomal enzymes. Mutant receptors contg. cytoplasmic domains of .gtoreq.29 amino acids functioned normally in endocytosis, whereas a mutant receptor with a 28-amino acid cytoplasmic domain was internalized extremely slowly. Alanine scanning of the region between amino acids 19 and 30 identified tyrosine 26 and valine 29 as the most important residues for rapid receptor internalization. Tyrosine 24 and lysine 28 also contributed to the signal,whereas the other amino acids were not crit. The tyrosines could be substituted with phenylalanines with no loss of activity, indicating the requirement for an arom. residue in these positions rather than tyrosine specifically. Conservative substitutions of arginine or histidine for lysine 28 also preserved the internalization signal. Apparently, the sequence Tyr-Lys-Tyr-Ser-Lys-Val serves as the internalization signal for the mannose 6-phosphate/insulin-like growth factor-II receptor. The crucial elements of this sequence are present in the cytoplasmic tails of a no. of other membrane receptors and proteins known to undergo rapid internalization.

L16 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2001 ACS
1989:226099 Document No. 110:226099 The chicken liver cation-independent mannose 6-phosphate receptor lacks the high affinity binding site for insulin-like growth factor II. ***Canfield, William M.*** ; Kornfeld, Stuart (Sch. Med., Washington Univ., St. Louis, MO, 63110, USA). J. Biol. Chem., 264(13), 7100-3 (English) 1989. CODEN: JBCHA3. ISSN: 0021-9258.

AB The chicken liver cation-independence mannose 6-phosphate receptor was purified to apparent homogeneity by affinity chromatog. on pentamannose phosphate-Sepharose and tested for its ability to bind iodinated human insulin-like growth factor I (IGI-I), human IGF-II, and chicken IGF-II. In contrast to the bovine, rat, and human cation-independent mannose 6-phosphate receptors, which bind human IGF-II and IGF-I with nanomolar and micromolar affinities, resp., the chicken receptor failed to bind either radioligand at receptor concns. as high as 1 .mu.M. The bovine receptor binds chicken IGF-II with high affinity whereas the chicken receptor binds this ligand with only low affinity, which was estd. to be in the micromolar range. Thus, the chicken cation-independent mannose 6-phosphate receptor lacks the high-affinity binding site for IGF-II. These results provide an explanation for the failure of previous investigators to identify the type II IGF receptor by IGF-II crosslinking to chicken cells and indicate that the mitogenic activity of IGF-II in chick embryo fibroblasts is most likely mediated via the type I IGF receptor.

	L #	Hits	Search Text	DBs
1	L1	0	ACETYLGLUSOSAMINE ADJ4 PHOSPHOTRANSFERASE	USPAT ; US-PG PUB
2	L2	0	PHOSPHODIESTERASE ADJ3 ACEYTLGLUCOSAMINE	USPAT ; US-PG PUB
3	L3	0	3.1.4.45	USPAT ; US-PG PUB
4	L4	0	2.7.8.17	USPAT ; US-PG PUB
5	L5	2926	LYSOSOM$	USPAT ; US-PG PUB
6	L6	4093	HYDROLASE	USPAT ; US-PG PUB
7	L7	300	L5 AND L6	USPAT ; US-PG PUB
8	L8	0	MANNOSE ADJ 6 ADJ PHOSPHATE	USPAT ; US-PG PUB
9	L9	304	MANNOSE ADJ2 PHOSPHATE	USPAT ; US-PG PUB
10	L10	28	L9 AND L7	USPAT ; US-PG PUB

Title: US-09-635-872A-2

RESULT 1
Q9UK23
ID Q9UK23 PRELIMINARY; PRT; 515 AA.
AC Q9UK23;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE N-ACETYLGLUCOSAMINE-1-PHOSPHODIESTER ALPHA-N-ACETYLGLUCOSAMINIDASE
DE (EC 3.1.4.45).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20020246; PubMed=10551838;
RA Kornfeld R., Bao M., Brewer K., Noll C., Canfield W.M.;
RT "Molecular Cloning and Functional Expression of Two Splice Forms of
RT Human N-acetylglucosamine-1-phosphodiester alpha-N-
RT acetylglucosaminidase.";
RL J. Biol. Chem. 274:32778-32785(1999).
DR EMBL; AF187072; AAF08273.1; -.
DR HSSP; P04070; 1AUT.
DR InterPro; IPR000561; -.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 515 AA; 56153 MW; A56A6103C2D16809 CRC64;

Query Match 100.0%; Score 2827; DB 4; Length 515;
Best Local Similarity 100.0%; Pred. No. 2.2e-230;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MATSTGRWLLLRLALFGFLWEASGGLDSGASRDDDLLLPYPRARARLPRDCTRVRAGNRE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MATSTGRWLLLRLALFGFLWEASGGLDSGASRDDDLLLPYPRARARLPRDCTRVRAGNRE 60

Qy      61 HESWPPPPATPGAGGLAVRTFVSHFRDRAVAGHLTRAVEPLRTFSVLEPGGPGGCAARRR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 HESWPPPPATPGAGGLAVRTFVSHFRDRAVAGHLTRAVEPLRTFSVLEPGGPGGCAARRR 120

Qy     121 ATVEETARAADCRVAQNGGFFRMNSGECLGNVVSDERRVSSSGGLQNAQFGIRRDGTLVT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ATVEETARAADCRVAQNGGFFRMNSGECLGNVVSDERRVSSSGGLQNAQFGIRRDGTLVT 180

Qy     181 GYLSEEEVLDTENPFVQLLSGVVWLIRNGSIYINESQATECDETQETGSFSKFVNVISAR 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GYLSEEEVLDTENPFVQLLSGVVWLIRNGSIYINESQATECDETQETGSFSKFVNVISAR 240

Qy     241 TAIGHDRKGQLVLFHADGHTEQRGINLWEMAEFLLKQDVVNAINLDGGGSATFVLNGTLA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TAIGHDRKGQLVLFHADGHTEQRGINLWEMAEFLLKQDVVNAINLDGGGSATFVLNGTLA 300

Qy     301 SYPSDHCQDNMWRCPRQVSTVVCVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDEL 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 SYPSDHCQDNMWRCPRQVSTVVCVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDEL 360

Qy     361 DCGPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRRCKCEHHCPCDPKTGN 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 DCGPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRRCKCEHHCPCDPKTGN 420

Qy     421 CSVSRVKQCLQPPEATLRAGELSFFTRTAWLALTLALAFLLLISIAANLSLLLSRAERNR 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CSVSRVKQCLQPPEATLRAGELSFFTRTAWLALTLALAFLLLISIAANLSLLLSRAERNR 480

Qy     481 RLHGDYAYHPLQEMNGEPLAAEKEQPGGAHNPFKD 515
          |||||||||||||||||||||||||||||||||||||
Db     481 RLHGDYAYHPLQEMNGEPLAAEKEQPGGAHNPFKD 515
```

Title: US-09-635-872A-3

RESULT 1
AAY36229
ID AAY36229 standard; Protein; 306 AA.
XX
AC AAY36229;
XX
DT 17-SEP-1999 (first entry)
XX
DE Human secreted protein encoded by gene 6.
XX
KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS.
XX
OS Homo sapiens.
XX
PN WO9931117-A1.
XX
PD 24-JUN-1999.
XX
PF 17-DEC-1998; 98WO-US27059.
XX
PR 19-DEC-1997; 97US-0068369.
PR 18-DEC-1997; 97US-0068006.
PR 18-DEC-1997; 97US-0068007.
PR 18-DEC-1997; 97US-0068008.
PR 18-DEC-1997; 97US-0068053.
PR 18-DEC-1997; 97US-0068054.
PR 18-DEC-1997; 97US-0068057.
PR 18-DEC-1997; 97US-0068064.
PR 18-DEC-1997; 97US-0070923.
PR 19-DEC-1997; 97US-0068169.
PR 19-DEC-1997; 97US-0068365.
PR 19-DEC-1997; 97US-0068367.
PR 19-DEC-1997; 97US-0068368.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;
PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;
PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y;
PI Yu G;
XX
DR WPI; 1999-418749/35.
DR N-PSDB; AAX97921.
XX
PT New isolated human genes encoding secreted polypeptides
XX
PS Claim 11; Page 348-349; 537pp; English.
XX
CC AAX97916 to AAX98029 represent 110 isolated human secreted protein
CC genes. AAY36224 to AAY36727 represent the secreted proteins encoded by
CC the 110 human genes. The genes and their corresponding secreted
CC polypeptides are useful for preventing, treating or ameliorating medical
CC conditions, e.g. by protein or gene therapy. Also pathological conditions
CC can be diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new genes.
CC Specific uses are described for each of the 110 genes, based on which
CC tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, tumours, developmental
CC abnormalities and foetal deficiencies, blood disorders, diseases of the
CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's
CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,
CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular
CC disorders, kidney disorders, digestive/endocrine disorders, infections
CC and AIDS. The polypeptides are also useful for identifying their binding
CC partners. The sequences given in AAX97907 to AAX97915 and AAY36223 are
CC used in the exemplification of the present invention.
XX
SQ Sequence 306 AA;

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  Query Match             100.0%;  Score 1634;  DB 20;  Length 306;
  Best Local Similarity   100.0%;  Pred. No. 2e-161;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGVNNPFLPQASRLQAKRDPSPVSG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 maaglarllllglsaggpapagaakmkvveepnafgvnnpflpqasrlqakrdpspvsg 60

Qy     61 PVHLFRLSGKCFSLVESTYKYEFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 pvhlfrlsgkcfslvestykyefcpfhnvtqheqtfrwnaysgilgiwheweianntftg 120

Qy    121 MWMRDGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPLVCHPHALLVYPTL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 mwmrdgdacrsrsrqskvelacgksnrlahvsepstcvyaltfetplvchphallvyptl 180

Qy    181 PEALQRQWDQVEQDLADELITPQGHEKLLRTLFEDAGYLKTPEENEPTQLEGGPDSLGFE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 pealqrqwdqveqdladelitpqghekllrtlfedagylktpeeneptqleggpdslgfe 240

Qy    241 TLENCRKAHKELSKEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLRGDPG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 tlencrkahkelskeikrlkglltqhgipytrptetsnlehlghetprakspeqlrgdpg 300

Qy    301 LRGSL 305
          |||||
Db    301 lrgsl 305


RESULT   1
T45062
hypothetical protein c316G12.3 [imported] - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T45062
R;Frankland, J.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z22901
A;Accession: T45062
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-305 <FRA>
A;Cross-references: EMBL:AL031709; PIDN:CAB56184.1
A;Experimental source: clone LA16-316G12
C;Genetics:
A;Introns: 18/1; 37/2; 60/1; 78/2; 106/2; 137/3; 176/1; 203/3; 247/3; 275/1
A;Note: c316G12.3


  Query Match             100.0%;  Score 1634;  DB 2;  Length 305;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-132;
  Matches  305;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGVNNPFLPQASRLQAKRDPSPVSG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGVNNPFLPQASRLQAKRDPSPVSG 60

Qy     61 PVHLFRLSGKCFSLVESTYKYEFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PVHLFRLSGKCFSLVESTYKYEFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTG 120

Qy    121 MWMRDGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPLVCHPHALLVYPTL 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 MWMRDGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPLVCHPHALLVYPTL 180

Qy    181 PEALQRQWDQVEQDLADELITPQGHEKLLRTLFEDAGYLKTPEENEPTQLEGGPDSLGFE 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 PEALQRQWDQVEQDLADELITPQGHEKLLRTLFEDAGYLKTPEENEPTQLEGGPDSLGFE 240

Qy    241 TLENCRKAHKELSKEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLRGDPG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TLENCRKAHKELSKEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLRGDPG 300

Qy    301 LRGSL 305
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Db 301 LRGSL 305

Title: US-09-635-872A-3

RESULT 9
US-09-334-595-152
; Sequence 152, Application US/09334595
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/09/334,595
; CURRENT FILING DATE: 1999-06-17
; EARLIER APPLICATION NUMBER: PCT/US98/27059
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,007
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,057
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,006
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,369
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: 60/068,367
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: 60/068,169
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: 60/068,053
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,064
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,054
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,008
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/068,365
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 152
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (306)
; OTHER INFORMATION: Xaa equals stop translation
US-09-334-595-152

Query Match 100.0%; Score 1634; DB 17; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.1e-156;
Matches 305; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGVNNPFLPQASRLQAKRDPSPVSG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MAAGLARLLLLLGLSAGGPAPAGAAKMKVVEEPNAFGVNNPFLPQASRLQAKRDPSPVSG 60

Qy      61 PVHLFRLSGKCFSLVESTYKYEFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PVHLFRLSGKCFSLVESTYKYEFCPFHNVTQHEQTFRWNAYSGILGIWHEWEIANNTFTG 120

Qy     121 MWMRDGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPLVCHPHALLVYPTL 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 MWMRDGDACRSRSRQSKVELACGKSNRLAHVSEPSTCVYALTFETPLVCHPHALLVYPTL 180

Qy     181 PEALQRQWDQVEQDLADELITPQGHEKLLRTLFEDAGYLKTPEENEPTQLEGGPDSLGFE 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 PEALQRQWDQVEQDLADELITPQGHEKLLRTLFEDAGYLKTPEENEPTQLEGGPDSLGFE 240
```

```
Qy     241 TLENCRKAHKELSKEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLRGDPG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TLENCRKAHKELSKEIKRLKGLLTQHGIPYTRPTETSNLEHLGHETPRAKSPEQLRGDPG 300

Qy     301 LRGSL 305
           |||||
Db     301 LRGSL 305
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